

ABSTRACT OF THE DISCLOSURE

The present application relates to novel composite primers which make it possible to amplify in multiplex at a quantitative level of precision, and to the application of these composite primers for detecting gnomic rearrangements in general and cryptic chromosomal rearrangements in particular. These composite primers contain a tag the sequence of which is absent from or poorly represented in the genome analyzed, and which exhibits a very low propensity to form stable pairings. The composite primers, which contain them, make it possible to carry out multiplex amplifications with quantitative precision on the scale of a genome such as the human genome.